

FIRST EXPERIENCE ON BLUE GENE/L

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Blue Gene Applications Workshop

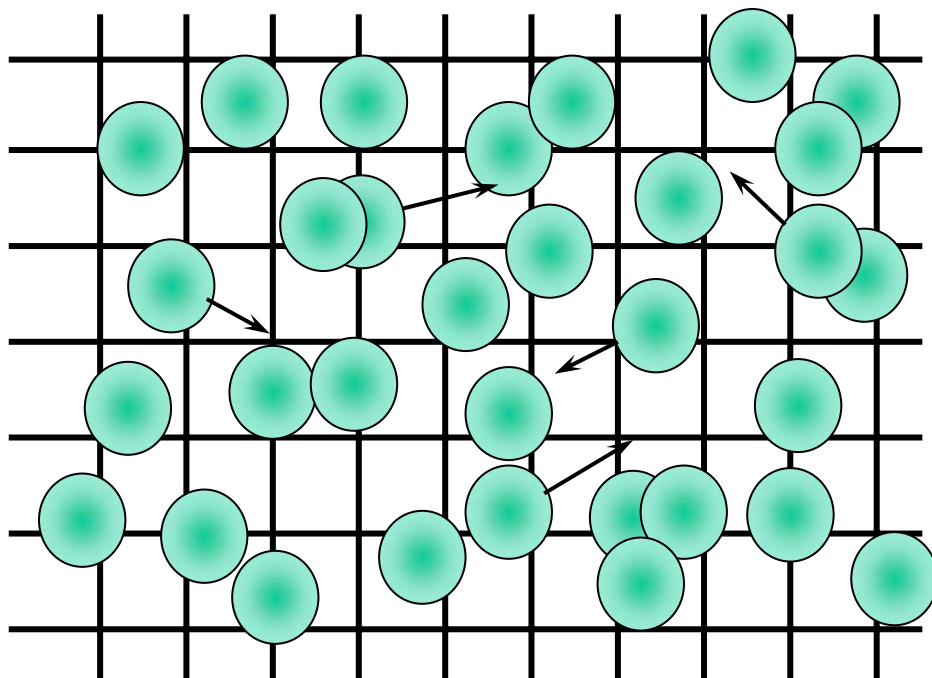
Argonne National Laboratory

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**Thanks to ANL MCS Andrew Siegel for helping me
port and run GTC on Blue Gene!!!**

GTC: a 3D gyrokinetic particle-in-cell (PIC) code in toroidal geometry

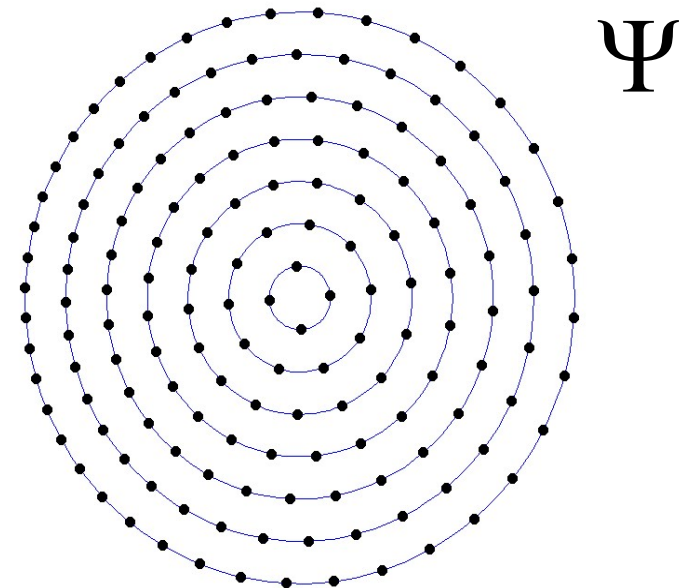
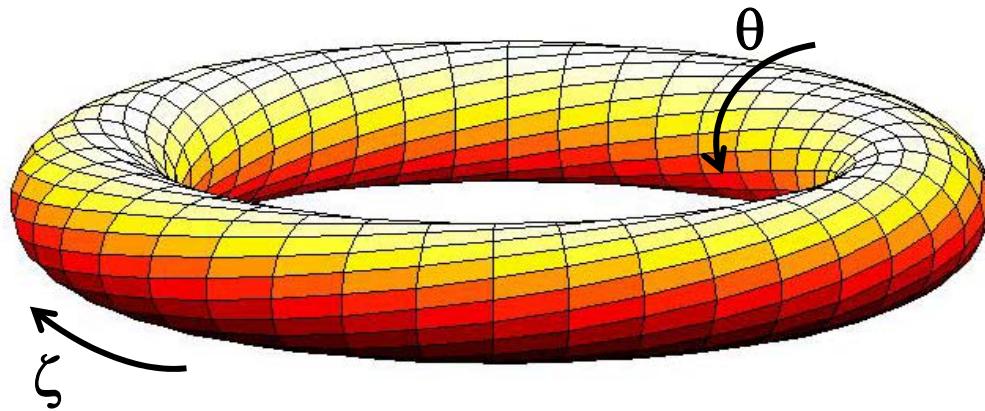
- Particles sample distribution function (markers).
- The particles interact via a grid, on which the potential is calculated from deposited charges.



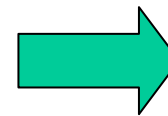
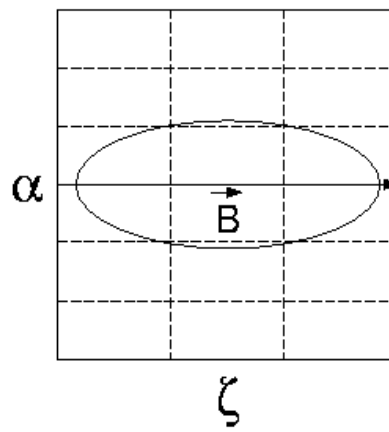
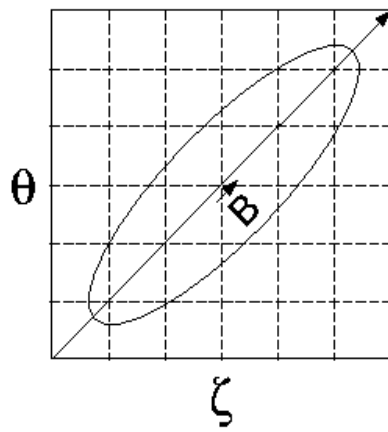
The PIC Steps

- “**SCATTER**”, or deposit, charges on the grid (nearest neighbors)
- Solve Poisson equation
- “**GATHER**” forces on each particle from potential
- Move particles (**PUSH**)
- Repeat...

GTC mesh and geometry: Field-line following coordinates



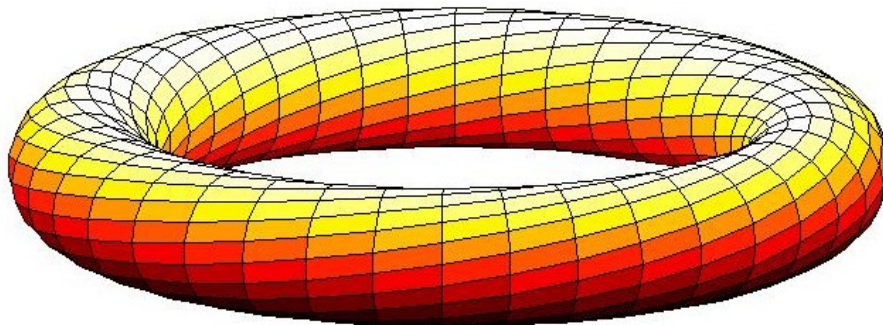
$$(\Psi, \alpha, \zeta) \Rightarrow \alpha = \theta - \zeta/q$$



Saves a factor of about
100 in CPU time

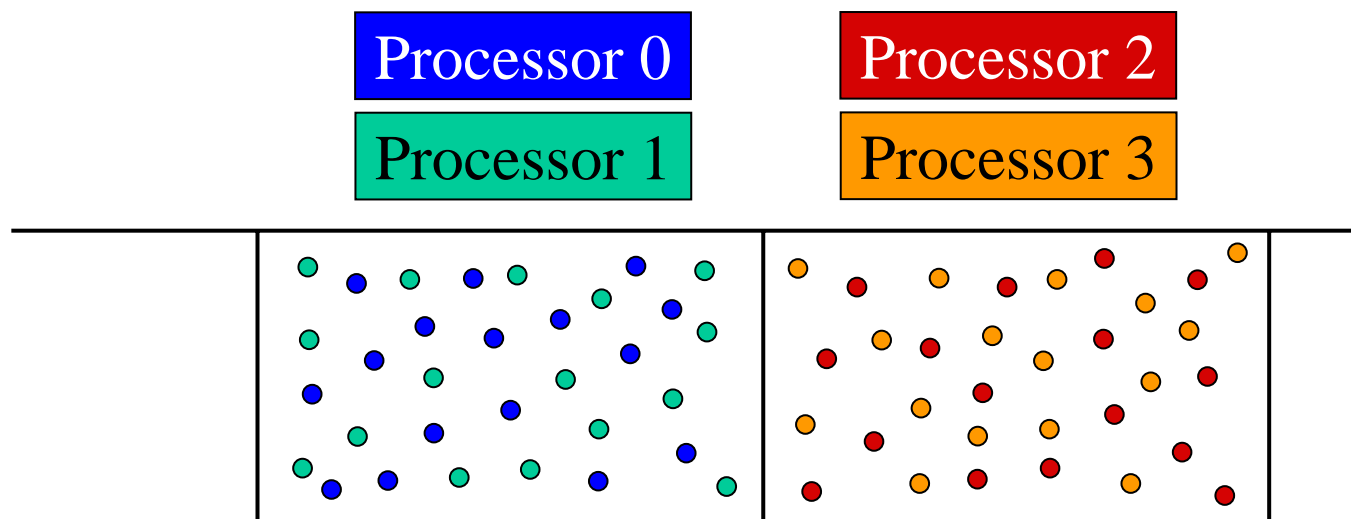
Domain Decomposition

- Domain decomposition:
 - each MPI process holds a toroidal section
 - each particle is assigned to a processor according to its position
- Initial memory allocation is done locally on each processor to maximize efficiency
- Communication between domains is nearest neighbors (MPI_Sendrecv calls).



MPI-based particle decomposition

- Each domain in the 1D (and soon 2D) domain decomposition can have more than 1 processor associated with it.
- Each processor holds a fraction of the total number of particles in that domain.

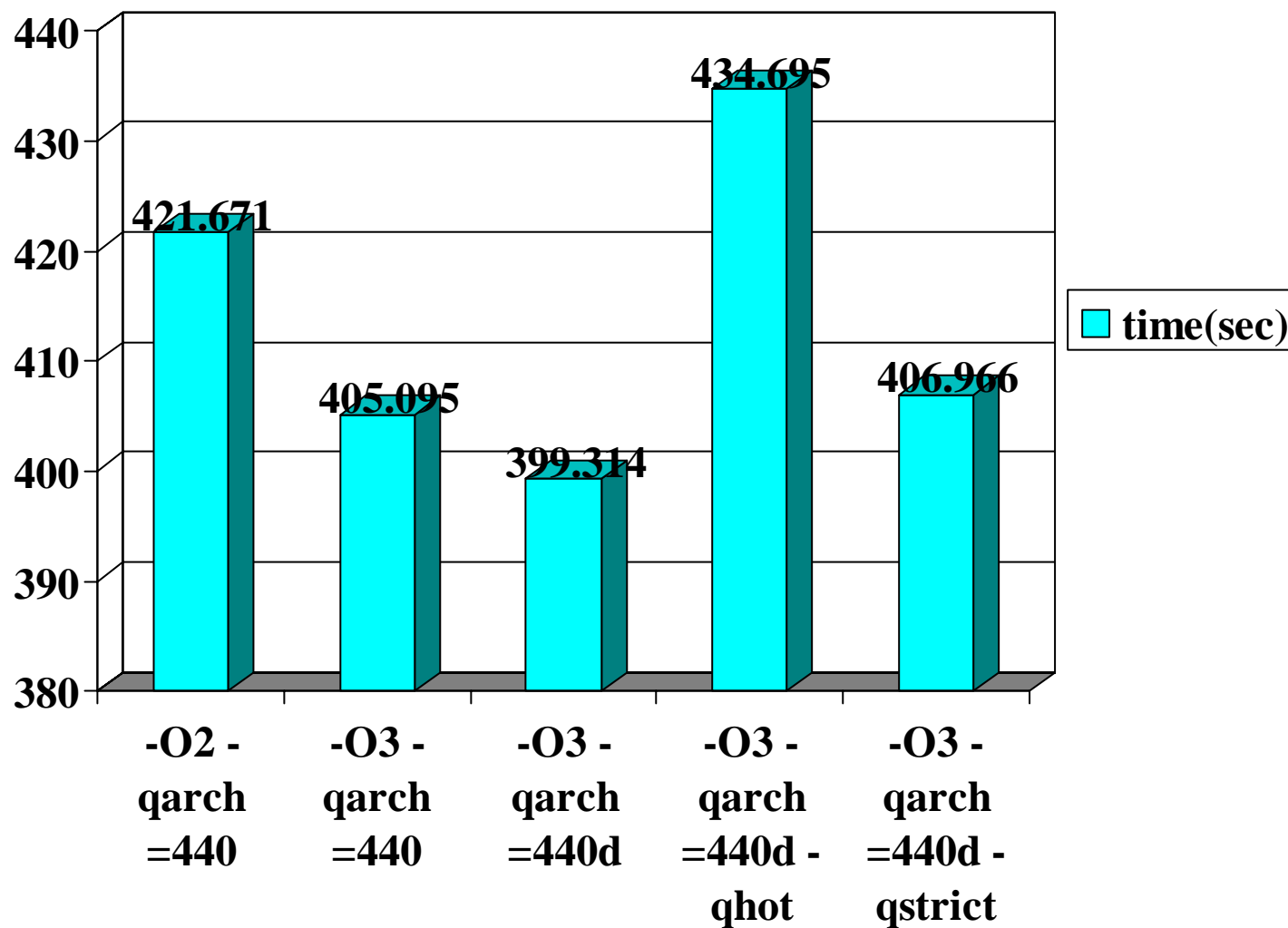


Compilation on Blue Gene/L

- Very easy... GTC is written in standard Fortran 90/95 and is being run routinely on NERSC's IBM SP P3.
- Only one issue
 - No MPI Fortran 90 module (cannot do “use mpi”)
 - Had to replace by “include ‘mpif.h’ “
- Best results with “-O3 -qarch=440d”
- “-qhot” was the slowest

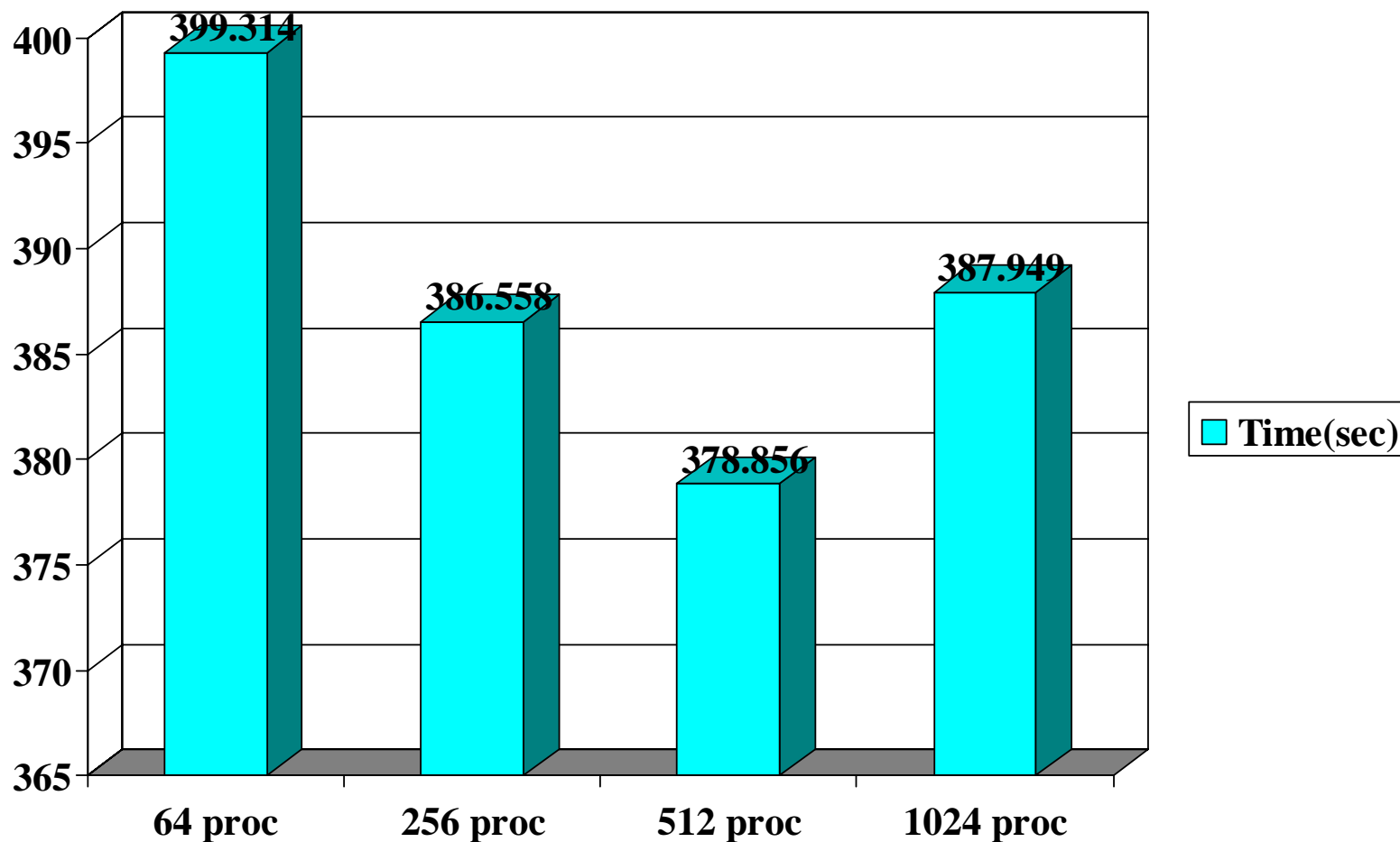
Compiler flags study

(tested with 64 processor run)



Weak scaling test: same number of particles per processor (~324,000)

64-processor test on Seaborg IBM P3 takes 390.017 sec



Things to know about MPI TRACE

- When running with MPI TRACE (libmpitrace.a), the code produces a maximum of 4 files:
 - mpi_profile.0 for rank 0 process
 - mpi_profile.# for the process with the MINIMUM comm.
 - mpi_profile.# for the process with the MAXIMUM comm.
 - mpi_profile.# for the process with the AVERAGE comm.
- This way, you get a maximum of 4 files even when running with 1,024 processors.
- I got this information from Bob Walkup...

Next steps

- Link with libmass.a and see if there is improvement
- Do a more thorough study of the communication timings.
- Learn about the mapping and see if I can take advantage of it.
- Do a full profiling of the code to compare with Seaborg or other platforms.
- Get access to a larger number of processors???